

About incoherent inference

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Approximate Bayesian Computation | Bayesian statistics | Bayesian model choice
| computational statistics

Abbreviations: ABC: approximate Bayesian Computation

In Templeton (2010), the Approximate Bayesian Computation (ABC) algorithm (see, e.g., Pritchard et al., 1999, Beaumont et al., 2002, Marjoram et al., 2003, Ratmann et al., 2009) is criticised on mathematical and logical grounds: “the [Bayesian] inference is mathematically incorrect and formally illogical”. Since those criticisms turn out to be bearing on Bayesian foundations rather than on the computational methodology they are primarily directed at, we endeavour to point out in this note the statistical errors and inconsistencies in Templeton (2010), referring to Beaumont et al. (2010) for a reply that is broader in scope since it also covers the phylogenetic aspects of nested clade versus a model-based approach.

Coherence

Templeton (2010) mostly uses arguments found in Templeton (2008) and already answered in Beaumont et al. (2010). However, the tone adopted in this PNAS paper is harsher and has a wider scope than in the earlier paper, in that it contains a foundational if inappropriate critical perspective on Bayesian model comparison. All of the arguments presented in Templeton’s tribute against the ABC “method” (Tavaré et al., 1997) actually aim at exposing the incoherence of the Bayesian approach. The major point of contention is that Bayes factors are mathematically incorrect because they contradict basic logic by being incoherent. The notion of coherence used in Templeton (2010) is borrowed from Lavine and Schervish (1999). Those authors introduced this notion to criticise Bayes factors in the limited sense that those may be nonmonotonous in the alternative hypothesis—in cases when monotony is relevant—and thus that posterior probabilities—which are coherent—should be used instead in a correct decision theoretic perspective.

Bayes factors

The core of the Bayesian paradigm is to incorporate all aspects of uncertainty within a prior distribution on the parameter space and all aspects of decision consequences within a loss function in order to produce a single inferential machine that provides the “optimal” solution (Berger, 1985). Posterior probabilities and hence Bayes factors (Kass and Raftery, 1995) are the product of this inferential machine when the goal is the selection of a statistical model. We recall that a Bayes factor, of the form

$$B_{12}^{\pi}(x) = \frac{\int_{\Theta_1} \pi_1(\theta_1) f_1(x|\theta_1) d\theta_1}{\int_{\Theta_2} \pi_2(\theta_2) f_1(x|\theta_2) d\theta_2} = \frac{m_1(x)}{m_2(x)},$$

compares the marginal likelihoods at the observed data x under both models under comparison. The suggestion of Templeton (2010) to “incorporate the sampling error of the observed statistic” is therefore exhibiting a misunderstanding of the above Bayesian construction since the posterior dis-

tributions naturally incorporate the sampling errors $f_1(x|\theta_1)$ and $f_2(x|\theta_2)$ under both models.

Templeton’s (2010) first argument against Bayes factors, namely that “the probability of the nested special case must be less than or equal to the probability of the general model within which the special case is nested. Any statistic that assigns greater probability to the special case is incoherent”, proceeds from the “natural” argument that larger models should have larger probabilities by an encompassing analogy. (Note that the notion of defining “the” probability over the collection of models that Templeton seems to take for granted does not make sense outside a Bayesian framework.) The author presents a Venn diagram to further explain why a larger set should have a larger measure, as if this simple-minded analogy was relevant in model choice settings. We found similar arguments in the recent epistemological book by Sober (2008) as well as in Popper (1959). This reductive viewpoint does not account for the fact that in Bayesian model choice, different models induce different parameters spaces and that those parameter spaces are endowed with orthogonal measures, especially if those spaces are of different dimensions. When the smaller parameter space corresponds to the restriction $\theta_1 = 0$, the measure of this constraint is zero in the larger space, i.e. $P(\theta_1 = 0|M_2) = 0$, when the parameter space is continuous. As stressed by Jeffreys (1939), testing for point null hypotheses (and hence for nested models) requires a drastic change of dominating measure so that both the null and the alternative hypotheses have a positive probability. This implies defining versions of the prior distribution over both parameter spaces. Therefore, talking of nested models having a “smaller” probability than the encompassing model or of “partially overlapping models” does not make sense from a measure theoretic (hence mathematical) perspective. In other words, the measure of the event is conditional on the model considered. (The fifty-one occurrences of the words *coherent* or *incoherent* in the paper do not bring additional scientific weight to the argument.)

Bayesian model comparison

When Templeton (2010) calls to logic for rejecting “incoherent” probability orderings on models, he rejects the fact that marginal likelihoods are in the same scale and can be added within the denominator of posterior probabilities, namely

$$\Pr(M_i|x) = \frac{\Pi_i m_i(x)}{\sum_{j=1}^k \Pi_j m_j(x)},$$

using standard notations (Berger, 1985, Robert, 2001). His argument is that the denominator is proportional to the probability of the union of several models and hence that the probabilities of the intersections of the overlapping hypotheses [or models] must be subtracted”. Another Venn diagram explains why this basic consequence of Bayes formula is “mathematically and logically incorrect” and why marginal likelihoods cannot be added up when models “overlap”. According to Templeton, “there can be no universal denominator, because a simple sum always violates the constraints of logic when logically overlapping models are tested”. Once more, this simply shows a poor understanding of the probabilistic modelling involved in model choice: The argument fails because

of the measure-theoretic assumptions separating models and because model choice ultimately involves the selection of one single model, hence the rejection of all other models. There cannot be a posterior weight on any intersection for this reason.

A second criticism of ABC (i.e. of the Bayesian approach) is that model choice requires a collection of models and cannot decide outside this finite and therefore incomplete collection. The very purpose of a Bayesian model choice procedure exactly aims at selecting the most likely model among all available, rather than rejecting a given model when the data is unlikely. Studies like Berger and Sellke (1987) have shown the difficulty of reasoning within a single model. Furthermore, Templeton (2010) advocates the use of a likelihood ratio test, which necessarily implies using two models with one nested within the other.

In this paper, Templeton also reiterates the earlier (2008) criticism that marginal likelihoods are not comparable across models, because they “are not adjusted for the dimensionality of the data or the models” (sic!). This point is missing the whole purpose of using marginal likelihoods, namely that they account for the dimensionality of the parameter by providing a natural Ockham’s razor (MacKay, 2002) penalising the larger model without requiring to specify a dimension penalty. Both BIC and DIC (Spiegelhalter et al., 2002) are approximations to the exact Bayesian evidence, which shows the intrinsic penalisation thus provided by marginal likelihoods. Note also that ABC applies the basic principles of a Bayesian model comparison to a summary statistic that is common across models (Grelaud et al., 2009), rather than using model specific summary statistics which would then be inconsistent.

Implications of model criticism

The point corresponding to the quote “ABC is used for parameter estimation in addition to hypothesis testing and another source of incoherence is suggested from the internal discrepancy between the posterior probabilities generated by ABC and the parameter estimates found by ABC” is that, while the posterior probability that $\theta_1 = 0$ (model M_1) is much higher than the posterior probability of the opposite (model M_2), the Bayes estimate of θ_1 under model M_2 is “significantly different from zero”. Again, this reflects both a misunderstanding of the probability model, namely that $\theta_1 = 0$ is impossible [has measure zero] under model M_2 , and a confusion between confidence intervals (that are model specific) and posterior probabilities (that work across models). The concluding message that “ABC is a deeply flawed Bayesian procedure in which ignorance overwhelms data to create massive incoherence” is thus unsubstantiated.

ABC is only a Monte Carlo scheme

An issue common to all recent criticisms by Templeton (2008, 2010) is the misleading or misled confusion between the ABC method and the resulting Bayesian inference. For instance, Templeton distinguishes between the incoherence in the ABC model choice procedure from the incoherence in the Bayes factor, when ABC is used as a computational device to approximate the Bayes factor. In the current case, the Bayes factor can be directly derived from the ABC simulation since the (accepted or rejected) proposed values are simulated from $\pi(\theta)f(x|\theta)$ (modulo a numerical approximation effect). This does not turn the Bayes factor into an ABC or simulation-based quantity. There is therefore no inferential aspect linked

with ABC, *per se*, it is simply a numerical tool to approximate Bayesian procedures and, with enough computer power, the approximation can get as precise as one wishes.

One of the arguments in Templeton (2010) relies on the following representation of the “ABC equation” (sic!)

$$P(H_i|H, S^*) = \frac{G_i(\|S_i - S^*\|)\Pi_i}{\sum_{j=1}^n G_j(\|S_j - S^*\|)\Pi_j}$$

where S^* is the observed summary statistic, S_i is “the vector of expected (simulated) summary statistics under model i ” and “ G_i is a goodness-of-fit measure”. Templeton states that this “fundamental equation is mathematically incorrect in every instance (...) of overlap.” This representation of the ABC approximation is again misleading or misled in that the simulation algorithm ABC produces an approximation to a posterior sample from $\pi_i(\theta_i|S^*)$. The resulting approximation to the marginal likelihood under model M_i is a regular Monte Carlo step that replaces an integral with a weighted sum (an average), not a “goodness-of-fit measure” and the S_i ’s are replicated many times. The subsequent argument of Templeton’s about the goodness-of-fit measures being “not adjusted for the dimensionality of the data” (re-sic!) and the resulting incoherence is therefore void of substance. The following argument repeats an misunderstanding stressed above with the probabilistic model involved in Bayesian model choice: the reasoning that, if

$$\sum_j \Pi_j = 1$$

“the constraints of logic are violated [and] the prior probabilities used in the very first step of their Bayesian analysis are incoherent”, does not assimilate the issue of measures over mutually exclusive spaces.

In Templeton (2010), ABC is presented as allowing statistical comparisons among simulated models: “ABC assigns posterior probabilities to a finite set of simulated a priori models.” The simulation aspect is treated with suspicion and opposed to “standard classical tests”, even though the method is simply replacing an intractable integral with a converging average. Once more, there is no statistical flaw that can be attributed to ABC since this is a purely numerical method. The models under comparison are therefore the same as those studied by “standard classical tests” and what is simulated is a sample from the posterior distribution associated with this model, not the model itself.

ACKNOWLEDGMENTS. This work was partly supported by the Agence Nationale de la Recherche (ANR, 212, rue de Bercy 75012 Paris) through the 2009 project ANR-08-BLAN-0218 BigMC and the 2009 project ANR-09-BLAN-01 EMILE.

References

- BEAUMONT, M., NIELSEN, R., ROBERT, C., HEY, J., GAGGIOTTI, O., KNOWLES, L., ESTOUP, A., MAHESH, P., CORANDERS, J., HICKERSON, M., SISSON, S., FAGUNDES, N., CHIKHI, L., BEERLI, P., VITALIS, R., CORNUET, J.-M., HUELSENBECK, J., FOLL, M., YANG, Z., ROUSSET, F., BALDING, D. and EXCOFFIER, L. (2010). In defense of model-based inference in phylogeography. *Molecular Ecology*, **19**(3) 436–446.
- BEAUMONT, M., ZHANG, W. and BALDING, D. (2002). Approximate Bayesian computation in population genetics. *Genetics*, **162** 2025–2035.
- BERGER, J. (1985). *Statistical Decision Theory and Bayesian Analysis*. 2nd ed. Springer-Verlag, New York.
- BERGER, J. and SELLKE, T. (1987). Testing a point-null hypothesis: the irreconcilability of significance levels and ev-

- idence (with discussion). *J. American Statist. Assoc.*, **82** 112–122.
- GRELAUD, A., MARIN, J.-M., ROBERT, C., RODOLPHE, F. and TALLY, F. (2009). Likelihood-free methods for model choice in gibbs random fields. *Bayesian Analysis*, **3(2)** 427–442.
- JEFFREYS, H. (1939). *Theory of Probability*. 1st ed. The Clarendon Press, Oxford.
- KASS, R. and RAFTERY, A. (1995). Bayes factors. *J. American Statist. Assoc.*, **90** 773–795.
- LAVINE, M. and SCHERVISH, M. J. (1999). Bayes factors: What they are and what they are not. *American Statist.*, **53** 119–122.
- MACKEY, D. J. C. (2002). *Information Theory, Inference & Learning Algorithms*. Cambridge University Press, Cambridge, UK.
- MARJORAM, P., MOLITOR, J., PLAGNOL, V. and TAVARÉ, S. (2003). Markov chain Monte Carlo without likelihoods. *Proc. Natl. Acad. Sci. USA*, **100** 15324–15328.
- POPPER, K. (1959). *Logic of Scientific Discovery*. Hutchinson, London.
- PRITCHARD, J., SEIELSTAD, M., PEREZ-LEZAUN, A. and FELDMAN, M. (1999). Population growth of human Y chromosomes: a study of Y chromosome microsatellites. *Mol. Biol. Evol.*, **16** 1791–1798.
- RATMANN, O., ANDRIEU, C., WIUJF, C. and RICHARDSON, S. (2009). Model criticism based on likelihood-free inference, with an application to protein network evolution. *PNAS*, **106** 1–6.
- ROBERT, C. (2001). *The Bayesian Choice*. 2nd ed. Springer-Verlag, New York.
- SOBER, E. (2008). *Evidence and Evolution*. Cambridge University Press, Cambridge.
- SPIEGELHALTER, D. J., BEST, N. G., CARLIN, B. P. and VAN DER LINDE, A. (2002). Bayesian measures of model complexity and fit (with discussion). *J. Royal Statist. Society Series B*, **64** 583–639.
- TAVARÉ, S., BALDING, D., GRIFFITH, R. and DONNELLY, P. (1997). Inferring coalescence times from DNA sequence data. *Genetics*, **145** 505–518.
- TEMPLETON, A. (2008). Statistical hypothesis testing in intraspecific phylogeography: nested clade phylogeographical analysis vs. approximate Bayesian computation. *Molecular Ecology*, **18(2)** 319–331.
- TEMPLETON, A. (2010). Coherent and incoherent inference in phylogeography and human evolution. *Proc. National Academy of Sciences*, **107(14)** 6376–6381.